

#09

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RAW SEQUENCE LISTING

DATE: 02/21/2002

PATENT APPLICATION: US/09/935,799A

TIME: 12:47:44

Input Set : A:\032301.195.seq.ST25.txt

Output Set: N:\CRF3\02212002\I935799A.raw

ENTERED

3 <110> APPLICANT: MOCKEL, Bettina, et al.
 5 <120> TITLE OF INVENTION: NUCLEOTIDE SEQUENCES WHICH CODE FOR THE csta GENE
 7 <130> FILE REFERENCE: 032301 WD 195
 C--> 9 <140> CURRENT APPLICATION NUMBER: US/09/935,799A
 C--> 9 <141> CURRENT FILING DATE: 2002-02-07
 9 <160> NUMBER OF SEQ ID NOS: 7
 11 <170> SOFTWARE: PatentIn version 3.1
 13 <210> SEQ ID NO: 1
 14 <211> LENGTH: 2718
 15 <212> TYPE: DNA
 16 <213> ORGANISM: Corynebacterium glutamicum
 18 <220> FEATURE:
 19 <221> NAME/KEY: CDS
 20 <222> LOCATION: (200)..(2515)
 21 <223> OTHER INFORMATION:
 24 <400> SEQUENCE: 1

25	aggatggtat aaatcatctc tcaatgttac ttttccattg ttaagaatta acaactctcg	60
27	gtgatttgtc gcatacccag ctgtcaaaga tccgatcatc ggcatacaga aacacccatc	120
29	tggccgaact ttcctttttc tgcattgcatt tctgcacaca gtttctgccc gctgtttctg	180
31	cccgcgtgtt ctacgcata gtg gct ttg aaa cga ccc gaa gag aaa aca gta	232
32	Met Ala Leu Lys Arg Pro Glu Glu Lys Thr Val	
33	1 5 10	
35	aag atc gtg acc ata aaa cag act gac aac atc aat gac gat gat ttg	280
36	Lys Ile Val Thr Ile Lys Gln Thr Asp Asn Ile Asn Asp Asp Asp Leu	
37	15 20 25	
39	gtg tac agc aac gct act gac ctt cca gta ggc gtg aag aag tcc cct	328
40	Val Tyr Ser Asn Ala Thr Asp Leu Pro Val Gly Val Lys Lys Ser Pro	
41	30 35 40	
43	aaa atg tca ccg acc gcc cgc gtt ggt ctc ctt gtc ttt ggg gtt atc	376
44	Lys Met Ser Pro Thr Ala Arg Val Gly Leu Leu Val Phe Gly Val Ile	
45	45 50 55	
47	gcg gcg gtg ggt tgg gga gca atc gct ttc tcc cgt ggc gaa aca atc	424
48	Ala Ala Val Gly Trp Gly Ala Ile Ala Phe Ser Arg Gly Glu Thr Ile	
49	60 65 70 75	
51	aac tct gtg tgg ctg gtt ttg gcg gca gtt ggt tcc tat atc att gcg	472
52	Asn Ser Val Trp Leu Val Leu Ala Ala Val Gly Ser Tyr Ile Ile Ala	
53	80 85 90	
55	ttt tct ttc tat gcc cga ctg att gaa tac aaa gtt gtt aag ccg aaa	520
56	Phe Ser Phe Tyr Ala Arg Leu Ile Glu Tyr Lys Val Val Lys Pro Lys	
57	95 100 105	
59	gat cag cga gca acc ccg gcg gaa tac gtt aat gac ggc aag gac tat	568
60	Asp Gln Arg Ala Thr Pro Ala Glu Tyr Val Asn Asp Gly Lys Asp Tyr	
61	110 115 120	

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63 gtc cca acg gat cgt cgt gtg ctt ttt ggc cac cac ttt gca gct att      616
64 Val Pro Thr Asp Arg Arg Val Leu Phe Gly His His Phe Ala Ala Ile
65      125                      130                      135
67 gca ggt gcc ggt cca ttg gtt gga cct gtc atg gcc gcg cag atg ggc      664
68 Ala Gly Ala Gly Pro Leu Val Gly Pro Val Met Ala Ala Gln Met Gly
69 140                      145                      150                      155
71 tac ctg cca ggc acc ttg tgg att atc ctc ggt gtg att ttc gcc ggt      712
72 Tyr Leu Pro Gly Thr Leu Trp Ile Ile Leu Gly Val Ile Phe Ala Gly
73      160                      165                      170
75 gca gtg cag gac tac cta gtg ctg tgg gtg tct act cgt agg cgt gga      760
76 Ala Val Gln Asp Tyr Leu Val Leu Trp Val Ser Thr Arg Arg Arg Gly
77      175                      180                      185
79 cgc tca ctt ggc cag atg gtt cgt gat gaa atg ggc acg gtc ggt gga      808
80 Arg Ser Leu Gly Gln Met Val Arg Asp Glu Met Gly Thr Val Gly Gly
81      190                      195                      200
83 gct gcc ggt atc ttg gcg acc atc tcc atc atg atc atc att atc gcg      856
84 Ala Ala Gly Ile Leu Ala Thr Ile Ser Ile Met Ile Ile Ile Ile Ala
85      205                      210                      215
87 gtg ctc gca ttg atc gtg gtt aat gca ctg gct gat tca cca tgg ggc      904
88 Val Leu Ala Leu Ile Val Val Asn Ala Leu Ala Asp Ser Pro Trp Gly
89 220                      225                      230                      235
91 gtt ttc tcc atc acc atg acc atc cca att gca ctg ttc atg ggt gtg      952
92 Val Phe Ser Ile Thr Met Thr Ile Pro Ile Ala Leu Phe Met Gly Val
93      240                      245                      250
95 tac ttg cgt tac ctg cgc cca ggt cgt gtt act gaa gtg tcc atc atc      1000
96 Tyr Leu Arg Tyr Leu Arg Pro Gly Arg Val Thr Glu Val Ser Ile Ile
97      255                      260                      265
99 ggt gtg gca ctg ctc ctg ctg gct atc gtt gct ggt ggt tgg gtt gca      1048
100 Gly Val Ala Leu Leu Leu Leu Ala Ile Val Ala Gly Gly Trp Val Ala
101      270                      275                      280
103 gac acc tca tgg ggc gtg gaa tgg ttc acc tgg tct aag acc act ttg      1096
104 Asp Thr Ser Trp Gly Val Glu Trp Phe Thr Trp Ser Lys Thr Thr Leu
105      285                      290                      295
107 gcg ttg gcc ttg atc ggt tac gga atc atg gct gcg att ttg ccg gtg      1144
108 Ala Leu Ala Leu Ile Gly Tyr Gly Ile Met Ala Ala Ile Leu Pro Val
109 300                      305                      310                      315
111 tgg ctg ctg ctt gca ccg cgc gat tac ctg tct acc ttt atg aag atc      1192
112 Trp Leu Leu Leu Ala Pro Arg Asp Tyr Leu Ser Thr Phe Met Lys Ile
113      320                      325                      330
115 ggc gtc atc ggt ctg ttg gca gtg ggt att ttg ttc gca cgt cct gag      1240
116 Gly Val Ile Gly Leu Leu Ala Val Gly Ile Leu Phe Ala Arg Pro Glu
117      335                      340                      345
119 gtg cag atg cct tcc gtg acc tcc ttc gca ctt gag ggc aac ggt ccg      1288
120 Val Gln Met Pro Ser Val Thr Ser Phe Ala Leu Glu Gly Asn Gly Pro
121      350                      355                      360
123 gtg ttc tct gga agt ctg ttc cca ttc ctg ttc atc acg att gcc tgt      1336
124 Val Phe Ser Gly Ser Leu Phe Pro Phe Leu Phe Ile Thr Ile Ala Cys
125      365                      370                      375
127 ggt gca ctg tct ggt ttc cac gca ctg att tct tca gga acc aca cca      1384

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128 Gly Ala Leu Ser Gly Phe His Ala Leu Ile Ser Ser Gly Thr Thr Pro
129 380                               385                               390                               395
131 aag ctt gtg gag aag gaa tcc cag atg cgc atg ctc ggc tac ggc ggc      1432
132 Lys Leu Val Glu Lys Glu Ser Gln Met Arg Met Leu Gly Tyr Gly Gly
133                               400                               405                               410
135 atg ttg atg gaa tct ttc gtg gcg atg atg gca ctg atc acc gct gtt      1480
136 Met Leu Met Glu Ser Phe Val Ala Met Met Ala Leu Ile Thr Ala Val
137                               415                               420                               425
139 att ctg gat cgt cac ctg tac ttc tcc atg aac gct ccg ctg gca ctg      1528
140 Ile Leu Asp Arg His Leu Tyr Phe Ser Met Asn Ala Pro Leu Ala Leu
141                               430                               435                               440
143 act ggt gga gat cca gca acc gca gct gag tgg gtt aac tcc att ggg      1576
144 Thr Gly Gly Asp Pro Ala Thr Ala Ala Glu Trp Val Asn Ser Ile Gly
145                               445                               450                               455
147 ctg aca ggt gcg gat atc acc ccg gaa cag ctg tcg gaa gct gct gaa      1624
148 Leu Thr Gly Ala Asp Ile Thr Pro Glu Gln Leu Ser Glu Ala Ala Glu
149 460                               465                               470                               475
151 agt gtc gga gaa tcc act gtt att tcc cgt acc ggt ggc gca cca acc      1672
152 Ser Val Gly Glu Ser Thr Val Ile Ser Arg Thr Gly Gly Ala Pro Thr
153                               480                               485                               490
155 ttg gcg ttc ggt atg tct gaa atc ctc tcc gga ttc atc ggc ggc gct      1720
156 Leu Ala Phe Gly Met Ser Glu Ile Leu Ser Gly Phe Ile Gly Gly Ala
157                               495                               500                               505
159 gga atg aag gcg ttc tgg tac cac ttc gcc atc atg ttt gag gct ctg      1768
160 Gly Met Lys Ala Phe Trp Tyr His Phe Ala Ile Met Phe Glu Ala Leu
161                               510                               515                               520
163 ttc atc ctc act act gtg gat gca ggt act cgt gtg gct cgc ttt atg      1816
164 Phe Ile Leu Thr Thr Val Asp Ala Gly Thr Arg Val Ala Arg Phe Met
165                               525                               530                               535
167 atg acc gat acc ttg ggc aat gtt cca ggt ctg cgc cgt ttc aag gat      1864
168 Met Thr Asp Thr Leu Gly Asn Val Pro Gly Leu Arg Arg Phe Lys Asp
169 540                               545                               550                               555
171 cct tca tgg act gtc ggt aac tgg att tct acc gtg ttt gtg tgt gct      1912
172 Pro Ser Trp Thr Val Gly Asn Trp Ile Ser Thr Val Phe Val Cys Ala
173                               560                               565                               570
175 cta tgg ggt gct att ttg ctc atg ggt gtt acc gat cca ctg ggc ggc      1960
176 Leu Trp Gly Ala Ile Leu Leu Met Gly Val Thr Asp Pro Leu Gly Gly
177                               575                               580                               585
179 atc aac gtg ctt ttc cca cta ttc ggt atc gct aac cag ctg ctc gcc      2008
180 Ile Asn Val Leu Phe Pro Leu Phe Gly Ile Ala Asn Gln Leu Leu Ala
181                               590                               595                               600
183 gct att gca ctt gct ctc gtg ctg gtt gtt gtg gtg aag aag ggc ctg      2056
184 Ala Ile Ala Leu Ala Leu Val Leu Val Val Val Lys Lys Gly Leu
185                               605                               610                               615
187 tac aag tgg gcg tgg att cca gct gtt cct ttg gca tgg gat ctc att      2104
188 Tyr Lys Trp Ala Trp Ile Pro Ala Val Pro Leu Ala Trp Asp Leu Ile
189 620                               625                               630                               635
191 gtc acg atg act gcg tca tgg cag aag att ttc cac tct gat ccg gct      2152
192 Val Thr Met Thr Ala Ser Trp Gln Lys Ile Phe His Ser Asp Pro Ala

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193          640          645          650
195 att ggc tac tgg gct cag aac gcg aac ttc cgc gat gca aag tct caa      2200
196 Ile Gly Tyr Trp Ala Gln Asn Ala Asn Phe Arg Asp Ala Lys Ser Gln
197          655          660          665
199 ggc ctt acc gaa ttt ggt gcc gct aaa tct cct gag gca atc gat gcg      2248
200 Gly Leu Thr Glu Phe Gly Ala Ala Lys Ser Pro Glu Ala Ile Asp Ala
201          670          675          680
203 gtt atc cga aac acc atg att cag ggc atc ttg tcc atc ctg ttc gcg      2296
204 Val Ile Arg Asn Thr Met Ile Gln Gly Ile Leu Ser Ile Leu Phe Ala
205          685          690          695
207 gtg ctc gtc ctc gtt gtt gtc ggc gca gcc att gcg gtg tgc atc aag      2344
208 Val Leu Val Leu Val Val Gly Ala Ala Ile Ala Val Cys Ile Lys
209 700          705          710          715
211 tcc atc agg gct cgt gca gcc gga aca cct ttg gag acc act gaa gag      2392
212 Ser Ile Arg Ala Arg Ala Ala Gly Thr Pro Leu Glu Thr Thr Glu Glu
213          720          725          730
215 cct gat act gaa tct gag ttc ttc gcc cca act gga ttc ctt gca tct      2440
216 Pro Asp Thr Glu Ser Glu Phe Phe Ala Pro Thr Gly Phe Leu Ala Ser
217          735          740          745
219 tcc agg gat aag gaa gtc cag gcc atg tgg gac gag cgc tac cca gcc      2488
220 Ser Arg Asp Lys Glu Val Gln Ala Met Trp Asp Glu Arg Tyr Pro Gly
221          750          755          760
223 ggt gcg ccc gtg tct tct gga ggg cac taaaacatga tggctcttac      2535
224 Gly Ala Pro Val Ser Ser Gly Gly His
225          765          770
227 tcatgcactg tggaaaatcc cgcggggcggt gtggtggtat ctcaactgagc tcatggggga      2595
229 cacggcgatat tccaagtatg tgggtgcactt aaagcaccac catccggatg ctccgattcc      2655
231 tactgagcgg gagtattggc gggcaaagta tgcagatcag gacgctaata ctggtgcccc      2715
233 ctg      2718
236 <210> SEQ ID NO: 2
237 <211> LENGTH: 772
238 <212> TYPE: PRT
239 <213> ORGANISM: Corynebacterium glutamicum
241 <400> SEQUENCE: 2
243 Met Ala Leu Lys Arg Pro Glu Glu Lys Thr Val Lys Ile Val Thr Ile
244 1          5          10          15
247 Lys Gln Thr Asp Asn Ile Asn Asp Asp Asp Leu Val Tyr Ser Asn Ala
248          20          25          30
251 Thr Asp Leu Pro Val Gly Val Lys Lys Ser Pro Lys Met Ser Pro Thr
252          35          40          45
255 Ala Arg Val Gly Leu Leu Val Phe Gly Val Ile Ala Ala Val Gly Trp
256          50          55          60
259 Gly Ala Ile Ala Phe Ser Arg Gly Glu Thr Ile Asn Ser Val Trp Leu
260 65          70          75          80
263 Val Leu Ala Ala Val Gly Ser Tyr Ile Ile Ala Phe Ser Phe Tyr Ala
264          85          90          95
267 Arg Leu Ile Glu Tyr Lys Val Val Lys Pro Lys Asp Gln Arg Ala Thr
268          100          105          110
271 Pro Ala Glu Tyr Val Asn Asp Gly Lys Asp Tyr Val Pro Thr Asp Arg

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272      115      120      125
275 Arg Val Leu Phe Gly His His Phe Ala Ala Ile Ala Gly Ala Gly Pro
276      130      135      140
279 Leu Val Gly Pro Val Met Ala Ala Gln Met Gly Tyr Leu Pro Gly Thr
280 145      150      155      160
283 Leu Trp Ile Ile Leu Gly Val Ile Phe Ala Gly Ala Val Gln Asp Tyr
284      165      170      175
287 Leu Val Leu Trp Val Ser Thr Arg Arg Arg Gly Arg Ser Leu Gly Gln
288      180      185      190
291 Met Val Arg Asp Glu Met Gly Thr Val Gly Gly Ala Ala Gly Ile Leu
292      195      200      205
295 Ala Thr Ile Ser Ile Met Ile Ile Ile Ala Val Leu Ala Leu Ile
296      210      215      220
299 Val Val Asn Ala Leu Ala Asp Ser Pro Trp Gly Val Phe Ser Ile Thr
300 225      230      235      240
303 Met Thr Ile Pro Ile Ala Leu Phe Met Gly Val Tyr Leu Arg Tyr Leu
304      245      250      255
307 Arg Pro Gly Arg Val Thr Glu Val Ser Ile Ile Gly Val Ala Leu Leu
308      260      265      270
311 Leu Leu Ala Ile Val Ala Gly Gly Trp Val Ala Asp Thr Ser Trp Gly
312      275      280      285
315 Val Glu Trp Phe Thr Trp Ser Lys Thr Thr Leu Ala Leu Ala Leu Ile
316      290      295      300
319 Gly Tyr Gly Ile Met Ala Ala Ile Leu Pro Val Trp Leu Leu Leu Ala
320 305      310      315      320
323 Pro Arg Asp Tyr Leu Ser Thr Phe Met Lys Ile Gly Val Ile Gly Leu
324      325      330      335
327 Leu Ala Val Gly Ile Leu Phe Ala Arg Pro Glu Val Gln Met Pro Ser
328      340      345      350
331 Val Thr Ser Phe Ala Leu Glu Gly Asn Gly Pro Val Phe Ser Gly Ser
332      355      360      365
335 Leu Phe Pro Phe Leu Phe Ile Thr Ile Ala Cys Gly Ala Leu Ser Gly
336      370      375      380
339 Phe His Ala Leu Ile Ser Ser Gly Thr Thr Pro Lys Leu Val Glu Lys
340 385      390      395      400
343 Glu Ser Gln Met Arg Met Leu Gly Tyr Gly Gly Met Leu Met Glu Ser
344      405      410      415
347 Phe Val Ala Met Met Ala Leu Ile Thr Ala Val Ile Leu Asp Arg His
348      420      425      430
351 Leu Tyr Phe Ser Met Asn Ala Pro Leu Ala Leu Thr Gly Gly Asp Pro
352      435      440      445
355 Ala Thr Ala Ala Glu Trp Val Asn Ser Ile Gly Leu Thr Gly Ala Asp
356      450      455      460
359 Ile Thr Pro Glu Gln Leu Ser Glu Ala Ala Glu Ser Val Gly Glu Ser
360 465      470      475      480
363 Thr Val Ile Ser Arg Thr Gly Gly Ala Pro Thr Leu Ala Phe Gly Met
364      485      490      495
367 Ser Glu Ile Leu Ser Gly Phe Ile Gly Gly Ala Gly Met Lys Ala Phe
368      500      505      510

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VERIFICATION SUMMARY

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L:9 M:270 C: Current Application Number differs, Replaced Current Application No

L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date